RAW SEQUE___E LISTING
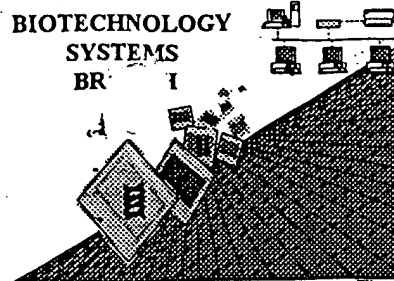# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____09|937,862_____

Source: _____PCT09_____

Date Processed by STIC: _____10|30|01_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/937,862

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ✓ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

PCT09

```
        RAW SEQUENCE LISTING            DATE: 10/30/2001
        PATENT APPLICATION:  US/09/937,862    TIME: 13:19:11

        Input Set : A:\W112887.txt
        Output Set: N:\CRF3\10302001\I937862.raw
```

**Does Not Comply
Corrected Diskette Needed**

```
W-->   4 <110> APPLICANT:
W-->   6       Oberste, M. Steven
W-->   7       Maher, Kaija
W-->   8       Kilpatrick, David R.
W-->   9       Pallansch, Mark A.
      12 <120> TITLE OF INVENTION: TYPING OF HUMAN NON-POLIO ENTEROVIRUSES
      14 <130> FILE REFERENCE: 14114.0353U2
C-->  16 <140> CURRENT APPLICATION NUMBER: US/09/937,862
C-->  16 <141> CURRENT FILING DATE: 2001-09-28
      16 <150> PRIOR APPLICATION NUMBER: PCT/US00/07828
W-->  17 <151> PRIOR FILING DATE: 2000-3-24
      19 <150> PRIOR APPLICATION NUMBER: 60/127,464
W-->  20 <151> PRIOR FILING DATE: 1999-3-31
      22 <160> NUMBER OF SEQ ID NOS: 86
      24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
      26 <210> SEQ ID NO: 1
      27 <211> LENGTH: 20
      28 <212> TYPE: DNA
      29 <213> ORGANISM: Artificial Sequence
W-->  31 <220> FEATURE:
W-->  31 <223> OTHER INFORMATION:
      31 <400> SEQUENCE: 1
      32  gcrtgcaatg ayttctcwgt                                    20
      34 <210> SEQ ID NO: 2
      35 <211> LENGTH: 18
      36 <212> TYPE: DNA
      37 <213> ORGANISM: Artificial Sequence
W-->  39 <220> FEATURE:
W-->  39 <223> OTHER INFORMATION:
      39 <400> SEQUENCE: 2
W-->  40  ngcnccdgat tgntgscc                                      18
      42 <210> SEQ ID NO: 3
      43 <211> LENGTH: 20
      44 <212> TYPE: DNA
      45 <213> ORGANISM: Artificial Sequence
      47 <220> FEATURE:
      48 <221> NAME/KEY: modified_base
      49 <222> LOCATION: (3)...(0)
      50 <223> OTHER INFORMATION: I
      52 <221> NAME/KEY: modified_base
      53 <222> LOCATION: (6)...(0)
      54 <223> OTHER INFORMATION: I
      56 <221> NAME/KEY: modified_base
      57 <222> LOCATION: (12)...(0)
      58 <223> OTHER INFORMATION: I
      60 <221> NAME/KEY: modified_base
      61 <222> LOCATION: (15)...(0)
```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

— must explain, see error summary sheet, Item 11 — Source ①

missing <221> must provide appropriate identifier <222> must give location of n & identify n → see error summary sheet item #9 ②

— same error Item 11

? unacceptable explanation → Item 11

RAW SEQUENCE LISTING   DATE: 10/30/2001
PATENT APPLICATION: US/09/937,862   TIME: 13:19:11

Input Set : A:\W112887.txt
Output Set: N:\CRF3\10302001\I937862.raw

Same errors as ① & ②

Repeated throughout

```
      62 <223> OTHER INFORMATION: I
      64 <400> SEQUENCE: 3
W--> 65  gcnccngayt gntgnccraa                                    20
      67 <210> SEQ ID NO: 4
      68 <211> LENGTH: 20
      69 <212> TYPE: DNA
      70 <213> ORGANISM: Artificial Sequence
      72 <220> FEATURE:
      73 <221> NAME/KEY: modified_base
      74 <222> LOCATION: (9)...(0)
      75 <223> OTHER INFORMATION: I
      77 <221> NAME/KEY: modified_base
      78 <222> LOCATION: (12)...(0)
      79 <223> OTHER INFORMATION: I
      81 <221> NAME/KEY: modified_base
      82 <222> LOCATION: (15)...(0)
      83 <223> OTHER INFORMATION: I
      85 <221> NAME/KEY: modified_base
      86 <222> LOCATION: (18)...(0)
      87 <223> OTHER INFORMATION: I
      89 <400> SEQUENCE: 4
W--> 90  atgtaygtnc cnccnggngg                                    20
      92 <210> SEQ ID NO: 5
      93 <211> LENGTH: 20
      94 <212> TYPE: DNA
      95 <213> ORGANISM: Artificial Sequence
      97 <220> FEATURE:
      98 <221> NAME/KEY: modified_base
      99 <222> LOCATION: (3)...(0)
     100 <223> OTHER INFORMATION: I
     102 <221> NAME/KEY: modified_base
     103 <222> LOCATION: (9)...(0)
     104 <223> OTHER INFORMATION: I
     106 <221> NAME/KEY: modified_base
     107 <222> LOCATION: (15)...(0)
     108 <223> OTHER INFORMATION: I
W--> 109 <400> SEQUENCE: 5
W--> 110  ggngcrttnc cytcngtcca                                   20
     112 <210> SEQ ID NO: 6
     113 <211> LENGTH: 20
     114 <212> TYPE: DNA
     115 <213> ORGANISM: Artificial Sequence
     117 <220> FEATURE:
     118 <221> NAME/KEY: modified_base
     119 <222> LOCATION: (6)...(0)
     120 <223> OTHER INFORMATION: I
     122 <221> NAME/KEY: modified_base
     123 <222> LOCATION: (8)...(0)
     124 <223> OTHER INFORMATION: I
```

RAW SEQUENCE LISTING   DATE: 10/30/2001
PATENT APPLICATION: US/09/937,862   TIME: 13:19:11

Input Set : A:\Wl12887.txt
Output Set: N:\CRF3\10302001\I937862.raw

```
126 <221> NAME/KEY: modified_base
127 <222> LOCATION: (9)...(0)
128 <223> OTHER INFORMATION: I
130 <221> NAME/KEY: modified_base
131 <222> LOCATION: (18)...(0)
132 <223> OTHER INFORMATION: I
134 <400> SEQUENCE: 6
W-(-> 135   acrtgncnng tytgcatngt                              20
137 <210> SEQ ID NO: 7
138 <211> LENGTH: 18
139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <221> NAME/KEY: modified_base
144 <222> LOCATION: (3)...(0)
145 <223> OTHER INFORMATION: I
147 <221> NAME/KEY: modified_base
148 <222> LOCATION: (15)...(0)
149 <223> OTHER INFORMATION: I
151 <400> SEQUENCE: 7
W--> 152   awnttytayg ayggntgg                                 18
154 <210> SEQ ID NO: 8
155 <211> LENGTH: 20
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <221> NAME/KEY: modified_base
161 <222> LOCATION: (3)...(0)
162 <223> OTHER INFORMATION: I
164 <221> NAME/KEY: modified_base
165 <222> LOCATION: (5)...(0)
166 <223> OTHER INFORMATION: I
168 <221> NAME/KEY: modified_base
169 <222> LOCATION: (6)...(0)
170 <223> OTHER INFORMATION: I
172 <221> NAME/KEY: modified_base
173 <222> LOCATION: (9)...(0)
174 <223> OTHER INFORMATION: I
176 <400> SEQUENCE: 8
W--> 177   tananngtnc ccatrttrtt                               20
179 <210> SEQ ID NO: 9
180 <211> LENGTH: 20
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <221> NAME/KEY: modified_base
186 <222> LOCATION: (9)...(0)
187 <223> OTHER INFORMATION: I
189 <221> NAME/KEY: modified_base
```

```
190 <222> LOCATION: (15)...(0)
191 <223> OTHER INFORMATION: I
193 <221> NAME/KEY: modified_base
194 <222> LOCATION: (18)...(0)
195 <223> OTHER INFORMATION: I
197 <400> SEQUENCE: 9
W--> 198   atgtayrtnc cnmcnggngc                                    20
200 <210> SEQ ID NO: 10
201 <211> LENGTH: 20
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <221> NAME/KEY: modified_base
207 <222> LOCATION: (3)...(0)
208 <223> OTHER INFORMATION: I
210 <221> NAME/KEY: modified_base
211 <222> LOCATION: (6)...(0)
212 <223> OTHER INFORMATION: I
214 <221> NAME/KEY: modified_base
215 <222> LOCATION: (12)...(0)
216 <223> OTHER INFORMATION: I
218 <221> NAME/KEY: modified_base
219 <222> LOCATION: (15)...(0)
220 <223> OTHER INFORMATION: I
222 <400> SEQUENCE: 10
W--> 223   ggnggnggrt cngtnakytt                                    20
225 <210> SEQ ID NO: 11
226 <211> LENGTH: 20
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <221> NAME/KEY: modified_base
232 <222> LOCATION: (3)...(0)
233 <223> OTHER INFORMATION: I
235 <221> NAME/KEY: modified_base
236 <222> LOCATION: (12)...(0)
237 <223> OTHER INFORMATION: I
239 <221> NAME/KEY: modified_base
240 <222> LOCATION: (15)...(0)
241 <223> OTHER INFORMATION: I
243 <400> SEQUENCE: 11
W--> 244   gangaraayc tnatngarac                                    20
246 <210> SEQ ID NO: 12
247 <211> LENGTH: 19
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <221> NAME/KEY: modified_base
253 <222> LOCATION: (6)...(0)
```

```
      254 <223> OTHER INFORMATION: I
      256 <221> NAME/KEY: modified_base
      257 <222> LOCATION: (12)...(0)
      258 <223> OTHER-INFORMATION  I
      260 <400> SEQUENCE: 12
W--> 261   cccatnakrt cnatrtccc                              19
      263 <210> SEQ ID NO: 13
      264 <211> LENGTH: 20
      265 <212> TYPE: DNA
      266 <213> ORGANISM: Artificial Sequence
      268 <220> FEATURE:
      269 <221> NAME/KEY: modified_base
      270 <222> LOCATION: (9)...(0)
      271 <223> OTHER INFORMATION  I
      273 <221> NAME/KEY: modified_base
      274 <222> LOCATION: (11)...(0)
      275 <223> OTHER INFORMATION  I
      277 <221> NAME/KEY: modified_base
      278 <222> LOCATION: (12)...(0)
      279 <223> OTHER INFORMATION: I
      281 <400> SEQUENCE: 13
W--> 282   gtretyacna nnagrtcyct                             20
      284 <210> SEQ ID NO: 14
      285 <211> LENGTH: 19
      286 <212> TYPE: DNA
      287 <213> ORGANISM: Artificial Sequence
W--> 289 <220> FEATURE:
W--> 289 <223> OTHER INFORMATION:
      289 <400> SEQUENCE: 14
      290   tsaarytgtg caargacac                              19
      292 <210> SEQ ID NO: 15
      293 <211> LENGTH: 18
      294 <212> TYPE: DNA
      295 <213> ORGANISM: Artificial Sequence
W--> 297 <220> FEATURE:
W--> 297 <223> OTHER INFORMATION:
      297 <400> SEQUENCE: 15
      298   stgyccagat ttcagtgt                               18
      300 <210> SEQ ID NO: 16
      301 <211> LENGTH: 20
      302 <212> TYPE: DNA
      303 <213> ORGANISM: Artificial Sequence
W--> 305 <220> FEATURE:
W--> 305 <223> OTHER INFORMATION:
      305 <400> SEQUENCE: 16
W--> 306   ggnacncayr tnathtggga                             20
      308 <210> SEQ ID NO: 17
      309 <211> LENGTH: 20
      310 <212> TYPE: DNA
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/937,862**

DATE: 10/30/2001
TIME: 13:19:12

Input Set : **A:\Wl12887.txt**
Output Set: **N:\CRF3\10302001\I937862.raw**

```
L:4    M:201 W: Mandatory field data missing, APPLICANT NAME
L:16   M:270 C: Current Application Number differs, Replaced Current Application No
L:16   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:17   M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:20   M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:31   M:258 W: Mandatory Feature missing, <220> FEATURE:
L:31   M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:39   M:258 W: Mandatory Feature missing, <220> FEATURE:
L:39   M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:40   M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:40   M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:40   M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:65   M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:90   M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:109  M:283 W: Missing Blank Line separator, <400> field identifier
L:110  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:135  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:152  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:177  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:198  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:223  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:244  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:261  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:282  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:289  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:289  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:297  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:297  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:305  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:305  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:306  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:306  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:306  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:327  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:352  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:377  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:402  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:423  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:448  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2022 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:81
L:2022 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:81
L:2022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81
L:2034 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:82
L:2034 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:82
L:2034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:2046 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:83
L:2046 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:83
L:2046 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83
```

VERIFICATION SUMMARY　　　　　　　DATE: 10/30/2001
PATENT APPLICATION:　**US/09/937,862**　　TIME: 13:19:12

Input Set : **A:\W112887.txt**
Output Set: **N:\CRF3\10302001\I937862.raw**

```
L:2058 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:84
L:2058 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:84
L:2058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:2083 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:86
L:2083 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:86
L:2083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86
```